RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/798,096*

Source: *+FWD~*

Date Processed by STIC: *3/22/04*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: /0/798, 096

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____Wrapped Nucleics **Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____Misaligned Amino **Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____Variable Length Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____PatentIn 2.0 **"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____Skipped Sequences **(OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____Skipped Sequences **(NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____Use of n's or Xaa's **(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____Invalid <213> **Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____PatentIn 2.0 **"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

SEQUENCE LISTING

[handwritten: Submitted file could not be processed due to numerous errors.]

<110> Rea-Min Chu

Ching-Yi Lin

Ya-Wen Hsiao

Kuang-Wen Liao

<120> COMPLEX IMMUNO-GENE MEDICAL COMPOSITION FOR INHIBITING TUMOR CELLS

<160> 4

<210> 1

<211> 636

<212> mRNA and PRT *[handwritten: delete, mandatory), <212> has to be either DNA, RNA OR PRT, if it is both DNA/RNA please use type DNA and explain in section <220>-<223>.]*

<213> Human *[handwritten: please insert <220> - please insert into section <223>.]*

<221> IL-6 *[handwritten: please insert into section <223>.]*

<300>

<308> NCBI pubmed Genbank ; Accession No. : NM_000600 *[handwritten: please insert dates for each accession No.]*

[handwritten: <309> ← please insert, mandatory), if <308> is shown than <309> must be inserted with response.]

<400> 1

63					78					93					108					
atg	aac	tcc	ttc	tcc	aca	agc	gcc	ttc	ggt	cca	gtt	gcc	tcc	tcc	ctg	ggg	ctg	ctc	ctg	60
Met	Asn	Ser	Phe	Ser	Thr	Ser	Ala	Phe	Gly	Pro	Val	Ala	Phe	Ser	Leu	Gly	Leu	Leu	Leu	
1				5					10					15					20	

123					138					153					168					
gtg	ttg	cct	gct	gcc	ttc	cct	gcc	cca	gta	ccc	cca	gga	gaa	gat	tcc	aaa	gat	gta	gcc	120
Val	Leu	Pro	Ala	Ala	Phe	Pro	Ala	Pro	Val	Pro	Pro	Gly	Glu	Asp	Ser	Lys	Asp	Val	Ala	
				25					30					35					40	

183					198					213					228					
gcc	cca	cac	aga	cag	cca	ctc	acc	tct	tca	gaa	cga	att	gac	aaa	caa	att	cgg	tac	atc	180
Ala	Pro	His	Arg	Gln	Pro	Leu	Thr	Ser	Ser	Glu	Arg	Ile	Asp	Lys	Gln	Ile	Arg	Tyr	Ile	
				45					50					55					60	

243					258					273					288					
ctc	gac	ggc	atc	tca	gcc	ctg	aga	aag	gag	aca	tgt	aac	aag	agt	aac	atg	tgt	gaa	agc	240
Leu	Asp	Gly	Ile	Ser	Ala	Leu	Arg	Lys	Glu	Thr	Cys	Asn	Lys	Ser	Asn	Met	Cys	Glu	Ser	
				65					70					75					80	

303					318					333					348					
agc	aaa	gag	gca	ctg	gca	gaa	aac	aac	ctg	aac	ctt	cca	aag	atg	gct	gaa	aaa	gat	gga	300
Ser	Lys	Glu	Ala	Leu	Ala	Glu	Asn	Asn	Leu	Asn	Leu	Pro	Lys	Met	Ala	Glu	Lys	Asp	Gly	
				85					90					95					100	

363					378					393					408					
tgc	ttc	caa	tct	gga	ttc	aat	gag	gag	act	tgc	ctg	gtg	aaa	atc	atc	act	ggt	ctt	ttg	360
Cys	Phe	Gln	Ser	Gly	Phe	Asn	Glu	Glu	Thr	Cys	Leu	Val	Lys	Ile	Ile	Thr	Gly	Leu	Leu	
				105					110					115					120	

423		438		453		468	

[handwritten: please see item #4 on error summary sheet.]

```
gag ttt gag gta tac cta cag tac ctc cag aac aga ttt gag agt agt gag gaa caa gcc   420
Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala
                125             130             135             140

483             498             513             528
aga gct gtg cag atg agt aca aaa gtc ctg atc cag ttc ctg cag aaa aag gca aag aat   480
Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn
                145             150             155             160

543             558             573             588
cta gat gca ata acc acc cct gac cca acc aca aat gcc agc ctg ctg acg aag ctg cag   540
Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln
                165             170             175             180

603             618             633             648
gca cag aac cag tgg ctg cag gac atg aca act cat ctc att ctg cgc agc ttt aag gag   600
Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu
                185             190             195             200

663             678             693
ttc ctg cag tcc agc ctg agg gct ctt cgg caa atg   636
Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met
                205             210
```

(handwritten: delete, see item #4 on error summary sheet.)

<210>2

<211>60   *(handwritten: delete, same error)*

<212>mRNA and PRT   *(handwritten: delete)*

<213>Human   *(handwritten: please insert)*

<220>

<221>IL-2 Signal Peptide   *(handwritten: please insert into section <223>)*

<300>

<308>NCBI pubmed Genbank ; Accession No. : V00564   *(handwritten: same error)*

<309>   *(handwritten: insert with response)*

<400>2
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atg tac agg atg caa ctc ctg tct tgc att gca cta agt ctt gca ctt gtc aca aac agt   60
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser
1           5           10          15          20
```

<210>3

<211>342   *(handwritten: delete, same error)*

<212>mRNA and PRT   *(handwritten: delete)*

<213>Human

<220>   *(handwritten: please insert)*

<221>Partial Sequence Encoding Human IL-15   *(handwritten: please move to section <223>.)*

<300>

<308>NCBI pubmed Genbank Accession No. : U14407 — *same error*

<309> ← *p/s insert*

<400>3

aac	tgg	gtg	aat	gta	ata	agt	gat	ttg	aaa	aaa	att	gaa	gat	ctt	att	caa	tct	atg	cat	60
Asn	Trp	Val	Asn	Val	Ile	Ser	Asp	Leu	Lys	Lys	Ile	Glu	Asp	Leu	Ile	Gln	Ser	Met	His	
1				5					10					15					20	

att	gat	gct	act	tta	tat	acg	gaa	agt	gat	gtt	cac	ccc	agt	tgc	aaa	gta	aca	gca	atg	120
Ile	Asp	Ala	Thr	Leu	Tyr	Thr	Glu	Ser	Asp	Val	His	Pro	Ser	Cys	Lys	Val	Thr	Ala	Met	
			25					30					35					40		

aag	tgc	ttt	ctc	ttg	gag	tta	caa	gtt	att	tca	ctt	gag	tcc	gga	gat	gca	agt	att	cat	180
Lys	Cys	Phe	Leu	Leu	Glu	Leu	Gln	Val	Ile	Ser	Leu	Glu	Ser	Gly	Asp	Ala	Ser	Ile	His	
				45					50					55					60	

gat	aca	gta	gaa	aat	ctg	atc	atc	cta	gca	aac	aac	agt	ttg	tct	tct	aat	ggg	aat	gta	240
Asp	Thr	Val	Glu	Asn	Leu	Ile	Ile	Leu	Ala	Asn	Asn	Ser	Leu	Ser	Ser	Asn	Gly	Asn	Val	
				65					70					75					80	

aca	gaa	tct	gga	tgc	aaa	gaa	tgt	gag	gaa	ctg	gag	gaa	aaa	aat	att	aaa	gaa	ttt	ttg	300
Thr	Glu	Ser	Gly	Cys	Lys	Glu	Cys	Glu	Glu	Leu	Glu	Glu	Lys	Asn	Ile	Lys	Glu	Phe	Leu	
				85					90					95					100	

cag	agt	ttt	gta	cat	att	gtc	caa	atg	ttc	atc	aac	act	tct							342
Gln	Ser	Phe	Val	His	Ile	Val	Gln	Met	Phe	Ile	Asn	Thr	Ser							
				105					110											

<210>4

<211>402

<212> mRNA and PRT — *delete, same error* *delete*

<213> Artificial Chimeric Sequence *delete*

<220>

<221> IL-2SP/IL-15MP — *move to section <223>,*

<223> Artificial Chimeric Sequence Encoding IL-2SP/IL-15MP

<300>

<308>NCBI pubmed Genbank IL-2 Accession No. : V00564
IL-15 Accession No. : U14407
— *please insert dates for each accession No.*

<309> ← *insert*

<400>4

atg	tac	agg	atg	caa	ctc	ctg	tct	tgc	att	gca	cta	agt	ctt	gca	ctt	gtc	aca	aac	agt	60
Met	Tyr	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu	Ser	Leu	Ala	Leu	Val	Thr	Asn	Ser	
1				5					10					15					20	

Sequence encoding IL-2signal peptide *delete*

aac	tgg	gtg	aat	gta	ata	agt	gat	ttg	aaa	aaa	att	gaa	gat	ctt	att	caa	tct	atg	cat	120
Asn	Trp	Val	Asn	Val	Ile	Ser	Asp	Leu	Lys	Lys	Ile	Glu	Asp	Leu	Ile	Gln	Ser	Met	His	
				25					30					35					40	

att	gat	gct	act	tta	tat	acg	gaa	agt	gat	gtt	cac	ccc	agt	tgc	aaa	gta	aca	gca	atg	180
Ile	Asp	Ala	Thr	Leu	Tyr	Thr	Glu	Ser	Asp	Val	His	Pro	Ser	Cys	Lys	Val	Thr	Ala	Met	
				45					50					55					60	

aag	tgc	ttt	ctc	ttg	gag	tta	caa	gtt	att	tca	ctt	gag	tcc	gga	gat	gca	agt	att	cat	240
Lys	Cys	Phe	Leu	Leu	Glu	Leu	Gln	Val	Ile	Ser	Leu	Glu	Ser	Gly	Asp	Ala	Ser	Ile	His	
				65					70					75					80	

gat	aca	gta	gaa	aat	ctg	atc	atc	cta	gca	aac	aac	agt	ttg	tct	tct	aat	ggg	aat	gta	300
Asp	Thr	Val	Glu	Asn	Leu	Ile	Ile	Leu	Ala	Asn	Asn	Ser	Leu	Ser	Ser	Asn	Gly	Asn	Val	
				85					90					95					100	

aca	gaa	tct	gga	tgc	aaa	gaa	tgt	gag	gaa	ctg	gag	gaa	aaa	aat	att	aaa	gaa	ttt	ttg	360
Thr	Glu	Ser	Gly	Cys	Lys	Glu	Cys	Glu	Glu	Leu	Glu	Glu	Lys	Asn	Ile	Lys	Glu	Phe	Leu	
				105					110					115					120	

cag	agt	ttt	gta	cat	att	gtc	caa	atg	ttc	atc	aac	act	tct	402
Gln	Ser	Phe	Val	His	Ile	Val	Gln	Met	Phe	Ile	Asn	Thr	Ser	
				125					130					